

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: November 5, 2001, 12:58:32 ; Search time 60.22 Seconds

(without alignments)  
466.762 Million cell updates/sec

Title: US-09-593-316-2

Perfect score: 2003

Sequence: 1 MNVKKVILSMILVSTIVIV.....IKLVKMSQTKENVNNV 369

Scoring table: BLASTOM62

Gapop 10.0 ; Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1906.5	95.2	368	2	A44785 N-acetylglucosamin
2	1711	85.4	371	2	146583 alpha-1,3-galactos
3	1705.5	85.1	376	2	A56480 N-acetylglucosamin
4	1519	75.8	371	2	149698 alpha-1,3-galactos
5	1471	73.4	394	2	A34417 alpha-1,3-mannosyl
6	673	33.6	295	2	PC1120 fucosylgalactose a
7	627	31.3	343	1	A14933 fucosylgalactose a
8	627	31.3	347	2	JC6126 alpha-N-
9	467	23.3	189	2	PC1168 histo-blood group
10	464.5	23.2	189	2	PC1165 histo-blood group
11	461.5	23.0	189	2	PC1166 histo-blood group
12	459.5	22.9	189	2	PC1173 histo-blood group
13	456.5	22.8	189	2	PC1169 histo-blood group
14	456.5	22.8	189	2	PC1170 histo-blood group
15	456.5	22.8	189	2	PC1171 histo-blood group
16	454.5	22.7	189	2	PC1172 histo-blood group
17	118	5.9	26	2	A39769 N-acetylglucosamin
18	110	5.5	505	2	A32261 aggrase (EC 3.2.1.
19	97.5	4.9	516	1	S44306 phenol 2-monooxyge
20	96	4.8	583	1	S40014 hypothetical prote
21	94.5	4.7	408	2	H64513 hypothetical prote
22	94.5	4.7	563	2	S58198 hypothetical prote
23	94.5	4.7	688	1	TYPTJ large T antigen
24	92.5	4.6	390	2	130395 probable transcrip
25	92	4.6	289	2	B81857 probable acetyltra
26	91.5	4.6	650	2	149523 tumor necrosis fac
27	91.5	4.6	817	2	086217 protein T2737.8 (1
28	91	4.5	297	2	113264 repressor protein
29	91	4.5	788	2	A71076 hypothetical prote

30	90.5	4.5	278	2	E86679 hypothetical prote
31	90.5	4.5	647	2	D25123 probable formate d
32	90	4.5	483	2	T05186 protein kinase F41
33	89.5	4.5	855	2	E71241 probable replicat
34	89.5	4.5	959	2	F72763 probable RNA-dir
35	89.5	4.5	1212	2	144051 hypothetical prote
36	89.5	4.5	1212	2	144236 hypothetical prote
37	89	4.4	466	2	T46054 hypothetical prote
38	89	4.4	699	2	S25541 heat shock protein
39	88.5	4.4	517	1	D37841 phenol 2-monooxyge
40	88	4.4	609	2	T14759 hypothetical prote
41	88	4.4	1307	2	H84467 hypothetical prote
42	88	4.4	3724	2	T18427 probable reticolen
43	87	4.3	533	2	T41382 acetylase - f1ss
44	87	4.3	536	1	008P7 head-to-tail joint
45	87	4.3	569	2	A43417 germ cell-less pro

#### ALIGNMENTS

RESULT 1  
A44785  
N-acetylglucosamine 3-alpha-galactosyltransferase (EC 2.4.1.124) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1993 #sequence, revision 19-Mar-1993 #text, Change 29-Sep-1999  
C:Accession: A44785  
R:Joziasse, D.H.; Shaper, J.H.; Van den Eljnden, D.H.; Van Tunen, A.J.; Shaper, N.L.  
J. Biol. Chem. 264, 14290-14297, 1989  
A:Title: Bovine alpha1-3-galactosyltransferase: isolation and characterization of a  
A:Reference number: A44785; M01D:89340543  
A:Accession: A44785  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-368 <J02>  
A:Superfamily: histo-blood group 1 transferase  
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match	95.2%	Score 1906.5;	DB 2;	Length 368;
Best local similarity	94.3%	Prod. No. 160-147;		
Matches 348;	Conservative 13;	Mismatches 7;	Indels 1;	Gaps 1;
QY	1	MNVKKVILSMILVSTIVIVEMVYHSPEGSFLWLNPSRNEVSGSS10KGMFPWFEN	60	
DB	1	MNVKKVILSMILVSTIVIVEMVYHSPEGSFLWLNPSRNEVSGSS10KGMFPWFEN	59	
QY	61	NGYQEDVDVDEHKQKQKSKLKLWPNDFKRPVVIMDKKAIWVGCTYKRAVL	120	
DB	60	NGYHEEDVDINEKQKQKQKSKLKLWPNDFKRPVVIMDKKAIWVGCTYKRAVL	119	
QY	121	DYAAOKITVGLTFAVGRYIEHIEFLTSANKHEMGHIVFVMDVDSRMLLEL	180	
DB	120	NYAAOKITVGLTFAVGRYIEHIEFLTSANKHEMGHIVFVMDVDSRMLLEL	179	
QY	181	PLRSFKVEVKPERKQVSVKRMKTIGEHTVANILOREVDLEGMVQVQVDFEVEITL	240	
DB	180	PLRSFKVEVKPERKQVSVKRMKTIGEHTVANILOREVDLEGMVQVQVDFEVEITL	239	
QY	241	GHSVQDQAMVYKADPDEFTYERKESAAVIPFGEGDYTYAAIPGCTPTOVANLLOET	300	
DB	240	GHSVQDQAMVYKADPDEFTYERKESAAVIPFGEGDYTYAAIPGCTPTOVANLLOET	299	
QY	301	KILDKKNDIEAOWHDSHLNKKPKLISPEYGMVHIGLPADIKLVKMSQTK	360	
DB	300	KILDKKNDIEAOWHDSHLNKKPKLISPEYGMVHIGLPADIKLVKMSQTK	359	
QY	361	EYNNVNNV 369		
DB	360	EYNNVNNV 368		

## RESULT 2

alpha-1,3-galactosyl transferase - pig

Accession: 146683

CDS: 21 Feb 1997 #sequence revision 21-Feb 1997 #text\_change 29-Sep-1999

CDS: 21 Feb 1997 #sequence revision 21-Feb 1997 #text\_change 29-Sep-1999

Accession: 146683

CDS: 21 Feb 1997 #sequence revision 21-Feb 1997 #text\_change 29-Sep-1999

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Query Match 85.4% Score 1711 DB 2 Length 371

Host Local Similarity 82.8% Pred. No. 1 to 131

Matches 309 Conservative 46 Mismatches 22 Indels 6 Gaps 3

Accession: 146683

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QY 238 ETLGSAVALQAWMYKADDFEYERKESAAVTPGGEDFYAAHFGSTPTVALNITO 297  
 DB 240 ETLGVALQAWMYKASERKTERRELSAAVTPGGEDFYAAHFGSTPTVALNITR 299  
 QY 298 ECFKGLDKKNDIEAQMDESHLNKRYFLNKPRTKLSPEYCWMDYHIGLPADIKLVKSM 357  
 DB 300 ECFKGLDKKNDIEAQMDESHLNKRYFLNKPRTKLSPEYCWMDYHIGLPADIKLVKSM 359  
 QY 358 QTKRYNNVANNV 369  
 DB 360 QTKRYNNVANNV 371

## RESULT 5

A34417  
 alpha-1,3-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.145)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 29-Sep-1999  
 C:Accession: A34417  
 R:Jansen, R.D.; Rajan, V.P.; Ruff, M.M.; Kukowska-Latallo, J.; Cummings, R.D.; Lowe, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 8227-8231, 1989  
 A:Title: Isolation of a cDNA encoding a murine UDPgalactose-beta-D-galactosyl-1,4-N-acetylglucosyltransferase  
 A:Reference number: A34417; MUID:90046769  
 A:Accession: A34417  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-394 <LAW>  
 A:Cross-references: GB:M28925; NID:q193419; PID:AAA37657.1; PID:q309242  
 C:Superfamily: histo-blood group 1 transferase  
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 73.4%; Score 1471; DB 2; Length 394;

Best Local Similarity 71.5%; Pred. No. 4.6e-112; Mismatches 43; Indels 16; Gaps 3;

QY 1 MNVKGKVIISMLVSAIVVFWETHSPPGSLFWINPSRNPVSGGSSIQCKMWFPPMFPN 60  
 DB 36 MANKKVVITIMLVSTVVVFWETV-----NRIPKV-GPNKKQKIMWPPSMFK 82  
 QY 61 NG---VDEDEVDDEKQKEDKSKLSDMFNPFKREVVNTDMKAPVWEGTYNKA 117  
 DB 83 NCTHSAVEENVGRRPKKGNCRLEPQLMDWFMFNKRRDVLTVPMKAPVWEGTYDPA 142  
 QY 118 VLDQYAKKIVGLTVAVGRITHTYLEELPTSAKNHMGHRYIFVWVDVSRMPLI 177  
 DB 143 LLEKYAIDIKLVGLTVAVGRITHTYLEELPTSAKNHMGHRYIFVWVDVSRMPLI 202  
 QY 178 ELGPIKSKRVFVKPRHMDVSMYRMKTIQGHIVAHIGREVDLFCMDVDVDPDDECV 237  
 DB 203 ILNPLHSIDVFEIRSKRWQDISMMKMKITGSHLAIHQHEVDPLFCMDVDVDPDDECV 262  
 QY 238 ETLGSAVALQAWMYKADDFEYERKESAAVTPGGEDFYAAHFGSTPTVALNITO 297  
 DB 263 ETLGVALQAWMYKASERKTERRELSAAVTPGGEDFYAAHFGSTPTVALNITR 322  
 QY 298 ECFKGLDKKNDIEAQMDESHLNKRYFLNKPRTKLSPEYCWMDYHIGLPADIKLVKSM 357  
 DB 323 ECFKGLDKKNDIEAQMDESHLNKRYFLNKPRTKLSPEYCWMDYHIGLPADIKLVKSM 382  
 QY 358 QTKRYNNVANNV 369  
 DB 383 QTKRYNNVANNV 394

## RESULT 6

PC1120  
 Nucleosylgalactose alpha-N-acetylglucosaminyltransferase (EC 2.4.1.40) A2 allele [valid]  
 N:Alternate names: histo-blood group A2 transferase  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Sep-2000  
 C:Accession: PC1120  
 R:Yamamoto, F.; McNeill, P.D.; Hakomori, S.

Biochem. Biophys. Res. Commun. 187, 366-374, 1992

A:Title: Human histo-blood group A2 transferase coded by A2 allele, one of the A subunit the catexyl terminal.  
 A:Reference number: PC1120; MUID:92392351  
 A:Accession: PC1120  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-295 <YAM>  
 A:Cross-references: GB:S44054; NID:q255066; PIRN:AAH2167.1; PIR:q255067  
 C:Superfamily: histo-blood group 1 transferase  
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 33.6%; Score 673; DB 2; Length 295;

Best Local Similarity 46.7%; Pred. No. 2.5e-47; Mismatches 128; Conservative 49; Mismatches 95; Indels 2; Gaps 2;

QY 95 RPEVNTDMKAPVWEGTYNKAVALDIYAAKQITVGTIVAVGRITHTYLEELPTSAKN 154  
 DB 1 RKDVLVTPWKLAPVWEGTYNKAVALDIYAAKQITVGTIVAVGRITHTYLEELPTSAKN 159  
 QY 155 HFMVGHRYIFVWVDVSRMPLIELGLPSFRVYEVKPRKQIVSWVRMKTIGEHIVAH 214  
 DB 60 HFMVGHRYIFVWVDVSRMPLIELGLPSFRVYEVKPRKQIVSWVRMKTIGEHIVAH 219  
 QY 215 IOREVDLFCMDVDVDPDDECVETLGSVALQAWMYKADDFEYERKESAAVTPG 274  
 DB 120 FLEVDYLVQVDMPEVDHGVETLPTFCTLPDCEGSSREAFYERKESAAVTPG 179  
 QY 275 EGDPEYAAHFGSTPTVALNITOEFKGLDKKNDIEAQMDESHLNKRYFLNKPRTK 344  
 DB 180 EGDPEYAAHFGSTPTVALNITOEFKGLDKKNDIEAQMDESHLNKRYFLNKPRTK 349  
 QY 335 SPEYCWMDYHIGLPADIKLVKSMQTKRYNNV 367  
 DB 240 SPEYCWMDYHIGLPADIKLVKSMQTKRYNNV 374

## RESULT 7

A34933  
 Nucleosylgalactose alpha-N-acetylglucosaminyltransferase (EC 2.4.1.40) A1 allele [valid]  
 N:Alternate names: alpha-3-N-acetylglucosaminyltransferase; blood-group substance A c; histo-blood group A glycosyltransferase  
 C:Species: Homo sapiens (man)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 08-Sep-2000  
 C:Accession: A34933; S095933; S13173; PC1164  
 R:Yamamoto, F.; Marken, J.; Tsui, T.; White, T.; Clausen, H.; Hakomori, S.  
 J. Biol. Chem. 265, 1146-1151, 1990  
 A:Title: Cloning and characterization of DNA complementary to human UDP-GalNAc: Fucal A:Reference number: A34933; MUID:90110098  
 A:Accession: A34933  
 A:Molecule type: mRNA  
 A:Residues: 1-353 <YAM1>  
 A:Cross-references: GB:J05175; NID:q340077; PID:AAA36792.1; PID:q340078  
 R:Yamamoto, F.I.; Clausen, H.; White, T.; Marken, J.; Hakomori, S.I.  
 Nature 345, 229-233, 1990  
 A:Title: Molecular genetic basis of the histo-blood group ABO system.  
 A:Reference number: S095933; MUID:90238543  
 A:Accession: S095933  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A:Molecule type: mRNA  
 A:Residues: 1-353 <YAM2>  
 R:Navaratnam, N.; Findlay, J.B.C.; Keen, J.N.; Watkins, W.M.  
 Biochem. J. 271, 93-98, 1990  
 A:Title: Purification, properties and partial amino acid sequence of the blood group A:Reference number: S13173; MUID:91024951  
 A:Accession: S13173  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 'X', 65-73, 'I', 76-77 <NAV>  
 R:Conlinto, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.  
 Biochem. Biophys. Res. Commun. 189, 154-164, 1992  
 A:Title: Animal histo-blood group ABO genes.

Accession number: pc1164; MIM:94080551  
 A:Accession: pc1164  
 A:Molecule type: DNA  
 A:Residues: 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

Query Match 44.58; Score 671; DB 1; Length 453;  
 Best Local Similarity 46.6%; Prev. No. 4, 70-47;  
 Matches 129; Conservative 50; Mismatches 94; Indels 4; Gaps 1;  
 92 DEKDFVVTMTAKRAVVEGTYNNAVADIVYAKOKITVGLTFVAVGRTLEITLFEETLS 151  
 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000.



